

		Query Match	48.3%;	Score 799.5;	DB 1;	Length 286;	
		Best Local Similarity	60.4%;	Pred. No. 1.9e-57;			
		Matches 166;	Conservative 39;	Mismatches 61;	Indels	9;	Gaps 4;
y	46	QNRKPELAGET-PRIVITSGKGVGKTTTANVGLSLARYGFSWAIDADLGLRNLDL	104				
b	4	QINKGEKKNSTDTRIVITSGKGVGKTTTANLGMSIARLYGYKVALIDADVGLRNLDL	63				
y	105	LIGLENRVNYTCVEINGDCRLDQALVRDKRWSNFELICISKPSKLPMFGGGKALEWLV	164				
b	64	LIGLENRVIIYTAMEVFEGECCLDQALIRDKRWSNLALLAISKTQRHYL--TRRMEMVLV	121				
y	165	DALKTRPESGPFIIIDCPAGIDAGITAITPANEAIVLTTPDTALRDADRVTGLCECD	224				

Db 122 DSTRLR---NVNFTLIDCPAGIDVCFVNAVAPAEAVVUTPTETISIRADRVACGLEAS 178
QY 225 GIRDIKMIVNRVTDMLKGDMMSVLDVQEMGLSLGLVIGEDSEVIRSTRNGFFLYLNK 284
Db 179 GIVEKLVNVRDPTQKNDMLSVRDVQEMGLGIPLLGAIIDNTNVIIVSTRNGOPLVNLK 238
QY 285 PPTLAGLAFEOAAWRLVRODSKAVMVEEPPKRG 319
Db 239 KTLUGSISFENAAARLV---GRKEYLVNLTGRNGK 270

RESULT 2

MIND_CHLVU STANDARD: PRT: 282 AA.
AC P36346;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN MIND.
OS Chlorella vulgaris.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TAM C-27 / TAMIYA;
RX MEDLINE=97303241; PubMed=9159184;
RA Takasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,
RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,
RA Inamura A., Yoshinaga K., Sugitani M.,
RT "Complete nucleotide sequence of the chloroplast genome from the
RT green alga Chlorella vulgaris: the existence of genes possibly
RT involved in chloroplast division."
RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997)
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC -!- DIVISION SITE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
CC -----
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CC -----
DR EMBL; AB001684; BAA57051.1;
DR InterPro; IPR000707; Para.
DR Pfam; PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Chloroplast.
FT NP_BIND 24 31 ATP (POTENTIAL).
SQ SEQUENCE 282 AA: 31013 MW: 94010DDA5A6AEC7 CRC64;

Query Match 47.9%; Score 792; DB 1; Length 282;
Best Local Similarity 60.4%; Pred. No. 7.4e-57;
Matches 165; Conservative 39; Mismatches 55; Indels 14; Gaps 5;

QY 59 RIVVITSGKGGVGTNTTANVGLSLARYGFSVVAIDAGLGNLDLLGLGNRVNVTQVE 118
Db 17 RVVITSGKGGVGTNTTANVGLSLARYGFSVVAIDAGLGNLDLLGLGNRVNVTQVE 76
QY 119 VINGCDRLDQALVRKRWNSFELLICISKPSKLPMPGFGKALEWLVDAKTRPESPDFI 178
Db 77 IVGQCRDLQALIRDKRWKLLALLAISKNQK--YNNTRKNMNLIDSVK---ELGQFV 131
QY 179 IIDCPAGIDAGFITAITPANEAVLVTTDPITALRDADRVTLGLLECDGIRDKIMVNRVT 238
Db 132 LIDCPAGIDVGFNATASAEAVIVTTPETAIRADRVAGLLEANGLYNNKLVNVRP 191
QY 239 DMKIGEDMMSVLDVQEMGLSLGLVIGEDSEVIRSTRNGFFLYLNKPTLAGLAFEOAAW 298

Db 192 DMKIONDMSVLDVQEMGLGIPLLGAIIDNTNVIIVSTRNGOPLVNLKTLGSLAFENAR 251
QY 299 RLV-EQDSKMKAYMVEEPPKRGFF-----SFFGK 326
Db 252 RLTKQD-----VFIDLTSPQKMPKLOEFFLG 280

RESULT 3

MIND_GUITH STANDARD: PRT: 269 AA.
AC 078436;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN MIND.
OS Guillardia theta (Cryptomonas phi).
OC Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, Guillardia theta:
RT complete sequence and conserved synteny groups confirm its common
RT ancestry with red algae."
RL J. Mol. Evol. 48:236-244(1999).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC -!- DIVISION SITE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
CC -----
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CC -----
DR EMBL; AF041468; AAC35621.1;
DR InterPro; IPR000707; Para.
DR Pfam; PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Chloroplast.
FT NP_BIND 10 17 ATP (POTENTIAL).
SQ SEQUENCE 269 AA: 29455 MW: BC363E954E689EA2 CRC64;

Query Match 42.0%; Score 694.5; DB 1; Length 269;
Best Local Similarity 55.9%; Pred. No. 5.1e-49;
Matches 146; Conservative 44; Mismatches 62; Indels 9; Gaps 3;

QY 59 RIVVITSGKGGVGTNTTANVGLSLARYGFSVVAIDAGLGNLDLLGLGNRVNVTQVE 118
Db 3 RVVITSGKGGVGTNTTANVGLSLARYGFSVVAIDAGLGNLDLLGLGNRVNVTQVE 62
QY 119 VINGCDRLDQALVRKRWNSFELLICISKPSKLPMPGFGKALEWLVDAKTRPESPDFI 178
Db 63 VLSGCRLEQALIKRQPNLVLLPAAQNRNK--DSVTEEQMKFLVNL----VNDYDYL 116
QY 179 IIDCPAGIDAGFITAITPANEAVLVTTDPITALRDADRVTLGLLECDGIRDKIMVNRVT 238
Db 117 LIDCPAGIETGFHNAIGPAQEAIVVTTETIAAYRADRVIGLLEANGIKQLLVNRLRP 176
QY 239 DMKIGEDMMSVLDVQEMGLSLGLVIGEDSEVIRSTRNGFFLYLNKPTLAGLAFEOAAW 298
Db 177 QMVKANDMMSVADVREILAIPLIGVPEDECIVSTRNGEPLVLEKLNLSPLGAFETAC 236
QY 299 RLVQEDSMKAYMVEEPPKRG 319
Db 237 RL---DGQEIFLDLQSYSG 254

```
RESULT 4
MIND_SYNY3
ID MIND_SYNY3 STANDARD; PRT; 266 AA.
AC Q55900;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).
GN MIND OR SLL0289.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN
CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
CC MATURE INTO POLAR Z RINGS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH MINC AND FTSZ (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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CC -----
CC EMBL; D64005; BAA10662.1; -
CC InterPro; IPR000392; NitrogenaseII.
CC InterPro; IPR000707; Para.
CC Pfam; PF00142; fer4_NifH; 1.
CC Pfam; PF00991; Para; 1.
CC Cell division; Septation; ATP-binding; Membrane; Complete proteome.
KW NP_BIND 10 17 ATP (POTENTIAL).
FT SEQUENCE 266 AA; 29047 MW; 4BC37880F086C9BF CRC64;
SQ
Query Match 38.9%; Score 643; DB 1; Length 266;
Best Local Similarity 52.8%; Pred. No. 7.1e-45;
Matches 130; Conservative 51; Mismatches 59; Indels 6; Gaps 2;
Qy 59 RIVVTSKGGVGGKTTTANVGLSLARYGFSVVAIDADLGLRLNLDLLGLNRYNYTCVE 118
Db 3 RIIVVTSKGGVGGKTTTANGLAARLKGKVVLDADFGRLNLDLLGLNRYNYTAID 62
Qy 119 VINGCDRLDQALVRDKRNSNFELLCISKRSLKPMFGGKALEWLVDALKTRPEGSPDT 178
Db 63 VLADCECTDKALVKDKRLPNLVLPAQRNSK--DAINAEQMSQSLVEQLKDK----FDVI 116
Qy 179 IIDCPAGIDAGFITATANEAVLVITTPDITRALDRVDTGLLECDGIRDIKMNVRVT 238
Db 117 IIDCPAGTEAGFRNVAFAQEAIIITTPMSAVRDVIGGLEADIDGKISLVNRLRP 176
Qy 239 DMKCEDMVLVDQVEMGLSLGLVPEDESVIRNTRGEPFLVLPKPTLAGLAFQAAW 298
Db 177 EMVQLNQMSIVEDILDLAVLGLIGILPDDQKIIISTNKGEPVLWEKLSVPGIAPQNIAR 236
Qy 299 RIVEQD 304
Db 237 RLEGQD 242
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RESULT 5
MIND_BACSU
ID MIND_BACSU STANDARD; PRT; 268 AA.
AC Q01464;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).
GN MIND OR DIVIVB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
MEDLINE=93015732; PubMed=1400225;
RA Varley A.W., Stewart G.C.;
RT "The divIVB region of the Bacillus subtilis chromosome encodes
RT homologs of Escherichia coli septum placement (minCD) and cell shape
RT (mreBCD) determinants.";
RL J. Bacteriol. 174:6729-6742(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=168;
MEDLINE=93211302; PubMed=8459776;
RA Lee S., Price C.W.;
RT "The minCD locus of Bacillus subtilis lacks the minE determinant that
RT provides topological specificity to cell division.";
RL Mol. Microbiol. 7:601-610(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015731; PubMed=1400224;
RA Levin P.A., Margolis P.S., Setlow P., Losick R., Sun D.;
RT "Identification of Bacillus subtilis genes for septum placement and
RT shape determination.";
RL J. Bacteriol. 174:6717-6728(1992).
CC -!- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN
CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
CC MATURE INTO POLAR Z RINGS (BY SIMILARITY).
CC -!- SUBUNIT: INTERACTS WITH MINC AND FTSZ (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
CC -!- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
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CC -----
CC EMBL; M95582; AAA22609.1; -
CC EMBL; Z15113; CAA78818.1; -
CC EMBL; M96343; AAA22401.1; -
CC EMBL; Z91118; CAB14759.1; -
CC PIR; S31205; S31205.
CC PIR; G45239; G45239.
CC PIR; F45240; F45240.
CC Subtilist; BG10330; minD.
CC InterPro; IPR000392; NitrogenaseII.
CC InterPro; IPR000707; Para.
CC Pfam; PF00142; fer4_NifH; 1.
CC Pfam; PF00991; Para; 1.
CC Cell division; Septation; ATP-binding; Membrane; Complete proteome.
KW NP_BIND 10 17 ATP (POTENTIAL).
FT SEQUENCE 268 AA; 29407 MW; 6665E9F693F58A9B CRC64;
SQ
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[illegible]

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DR EMBL; AE001468; AAD05905.1; -
DR InterPro; IPR000392; NitrogenaseII.
DR InterPro; IPR000707; Para.
DR Pfam; PF00142; fer4.NifH; 1.
DR Pfam; PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Membrane; Complete proteome.
FT NP_BIND 10 17 ATP (POTENTIAL).
SQ SEQUENCE 268 AA; 29265 MW; 1F479C187A201A63 CRC64;

Query Match 30.3%; Score 500.5; DB 1; Length 268;
Best Local Similarity 39.8%; Pred. No. 2.2e-33;
Matches 109; Conservative 65; Mismatches 81; Indels 19; Gaps 5;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGSVAIDALGLRLDLGLLENRVNYTCVEV 119
: ||||| ||||| ||||| : || | ||||| ||||| ||||| : ||||| : |||||
Db 4 VVITSGKGVGKSTTANLATGLAESGKVVAVDFDGLRLDLGLLENRVNYVDV 63
: ||||| ||||| ||||| : || | ||||| ||||| ||||| : ||||| : |||||
QY 120 INDCRLDQALYDRKWSFELLICISKPSKLPFGGKALEMLVDALKTRPEGSPDFII 179
: || ||||| ||||| : || | ||||| ||||| ||||| : ||||| : |||||
Db 64 MEKNCNLSQALITDKTKNLSELAASQSKDKNLDEKVAI--LINALR---ADFDYIL 117
: ||||| ||||| ||||| : || | ||||| ||||| ||||| : ||||| : |||||
QY 180 IDCPAGIDAGFTAITPANEAIVLTPDTALRDADRVTLGLEDGIR-----DIKMI 232
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 118 IDSPAGISGFHAIHLADMALVVTPEVSSLRSDRVIGIIDAISNRAKSGEEVHKHII 177
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
QY 233 VNRVDTMTKGDMSVLDVQVEMGLSLGLVPEDESEVIRSTNRGPPVLNKPPTLAGLA 292
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 178 INRLPELVANGEMISIEVLKILCLPLGIIPEDHIIISATNKGEPI--RTDCESAKA 235
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
QY 293 FQAAARWLVEQDSKAMVVEEPPKRGFFSFFGG 326
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 236 YQIRTRILGEE---VEYVEFKAKRGFFSALKG 265
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||

RESULT 8

ID MIND_ECOLI STANDARD; PRT; 269 AA.
AC P18197;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND).
GN MIND OR B1175.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89136010; PubMed=2645057;
RA de Boer P.A.J., Crossley R.E., Rothfield L.I.;
RT "A division inhibitor and a topological specificity factor coded for
RT by the minicell locus determine proper placement of the division
RT septum in E. coli."
RL Cell 56:641-649(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN-K12; PubMed=8905232;
RX Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE OF 1-12.
RC STRAIN-K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
RN [5]
RP FUNCTION AND MUTAGENESIS
RX MEDLINE=92097557; PubMed=1836760;
RA de Boer P.A.J., Crossley R.E., Hand A.R., Rothfield L.I.;
RT "The Mind protein is a membrane ATPase required for the correct
RT placement of the Escherichia coli division site."
RL EMBO J. 10:4371-4380(1991).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=99238467; PubMed=10220403;
RA Raskin D.M., de Boer P.A.;
RT "Rapid pole-to-pole oscillation of a protein required for directing
RT division to the middle of Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 96:4971-4976(1999).
CC -I- FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE. CELL DIVISION INHIBITORS MIND AND MIND ACT IN
CC CONCERT TO FORM AN INHIBITOR CAPABLE OF BLOCKING FORMATION OF THE
CC POLAR Z RING SEPTUMS. RAPIDLY OSCILLATES BETWEEN THE POLES OF THE
CC CELL TO DESTABILIZE FTSZ FILAMENTS THAT HAVE FORMED BEFORE THEY
CC MATURE INTO POLAR Z RINGS.
CC -I- SUBUNIT: INTERACTS WITH MIND AND FTSZ.
CC -I- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED.
CC -I- SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.

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CC EMBL; J03153; AAB59062.1; -
DR EMBL; AE000216; AAC74259.1; -
DR EMBL; D90751; BAA36009.1; -
DR EMBL; D90752; BAA36022.1; -
DR PIR; B31877; CCECID.
DR SWISS-2DPAGE; P18197; COLI.
DR EcoGene; EG10597; mind.
DR InterPro; IPR000707; Para.
DR Pfam; PF00991; Para; 1.
KW Cell division; Septation; ATP-binding; Inner membrane;
KW Complete proteome.
FT INIT_MET 0 0
FT NP_BIND 9 16 ATP (POTENTIAL).
FT MUTAGEN 14 14 G->S: LESS EFFECTIVE THEN WILD-TYPE.
FT MUTAGEN 15 15 K->Q: LOSS OF ACTIVITY.
FT MUTAGEN 15 16 KT->QR: LOSS OF ACTIVITY.
SQ SEQUENCE 269 AA; 29483 MW; 0D1B29A476A190B1 CRC64;

Query Match 29.0%; Score 479; DB 1; Length 269;
Best Local Similarity 39.9%; Pred. No. 1.2e-31;
Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;


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DR InterPro: IPR000707; Para.
DR Pfam: PF00142; fer4_NiH; 1.
DR Pfam: PF00991; Para; 1.
KW Hypothetical protein; ATP-binding; Complete proteome.
FT NP_BIND 10 17 ATP (POTENTIAL).
SO SEQUENCE 263 AA; 28950 MW; 292FDE38EE72AC4 CRC64;

Query Match 14.6%; Score 242; DB 1; Length 263;
Best Local Similarity 29.3%; Pred. NO. 1.6e-12;
Matches 77; Conservative 59; Mismatches 99; Indels 28; Gaps 9;

QY 60 IVVITSGGGVGGKTTTANVGLSLARYGFSVVAIDADLGLRNLDDLGLLENRYNYTCVEY 119
Db 5 IITIASGGVGGKTTTASLAVALLKGLVLAIDGDSMANLGLFNKRR-KPSLHEV 63

QY 120 INDCRLDQALVRD---KRWNFPELLQTSKPSKSLPMFGGKALEWLVDALKTRPEGSPD 176
Db 64 LS-----EADVRDAIYKHTGVVVL-----PTSLSLEGYKKSDDIDLLFDVYNEVADDF-D 113

QY 177 FIIDCPAGIDAGFITAITPANEAVLVTPDITARDADRVGTGLECDGIRDKIMVNRV 236
Db 114 VVIIDADAGLRNEMATHAIADKLLLVTPPEMFISIADAVRLKESAEAGTPLMGVVLNRV 173

QY 237 RTDMIKGEDMMSVLDYQEMLSLLGVIPEDSEVIRSNRGPFLY---LNKPEPTLAGLAF 293
Db 174 GRDF--GE--NGRDEIMLIGKVLVEPDENVRSALKMMSVIEYRKNSPAS----- 223

QY 294 EQAAWRLVEODSMKAVMVEEPK 316
Db 224 QATYKKLASIIAGVPIEDRIK 245

RESULT 13
YLXH_BACSU STANDARD; PRT; 298 AA.
AC P40742; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 33.2 KDA PROTEIN IN FLHF-CHEB INTERGENIC REGION (ORF298).
GN YLXH.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95078462; PubMed=7987014;
RA Kirsch M.L., Carpenter P.B., Ordal G.W.;
RT "A putative ATP-binding protein from the che/fla locus of Bacillus subtilis."
RL DNA Seq. 4:271-275(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X73682; CAA52034.1; -
CC EMBL: 299112; CAB13514.1; -
CC PIR: S34194; S34194.1; YLXH.
CC Subtilist; HG10254; YLXH.
DR InterPro: IPR000392; NitrogenaseI.
DR InterPro: IPR000707; Para.
DR Pfam: PF00142; fer4_NiH; 1.
DR Pfam: PF00991; Para; 1.
KW Hypothetical protein; ATP-binding; Complete proteome.
FT NP_BIND 39 46 ATP (POTENTIAL).
SQ SEQUENCE 298 AA; 33160 MW; AF6FE71FA3C1C972 CRC64;

Query Match 12.9%; Score 214; DB 1; Length 298;
Best Local Similarity 25.2%; Pred. No. 3.3e-10;
Matches 76; Conservative 56; Mismatches 119; Indels 50; Gaps 10;

QY 32 YNPNRSPRSPIRSYLOQENRK--PELAGETPRIVVITSGGGVGGKTTTANVGLSLARYGFS 89
Db 3 MNRVDOAAFLRAKMEKRRERVLDMVYSOKAKTLAVISGGVGGKSNITLNMALADOKGKK 62

QY 90 VVAIDADLGLRNLDDLGLLENRYNYTCVEVINGDCRLDQALYDRKRWNSFELLICISKPRS 149
Db 63 VLLIDLDGNGNIDILIG--NSSATIIDVLRKPLLOS-----S 102

QY 150 KLPMGF---GGKALE-----WLVDALKTRPESGP-DFIIIDCPAGIDAGFITAIT 193
Db 103 YGPKGLRYISGGTGLDVMFQDQRKWTFFANELSHALSQFDYVLFDMGAGLSKQDLPFIL 162

QY 196 PANEAVLVTPDITARDADRVGTGLECDGIRDKIMVNRVTPDMIKGEDMMS----- 248
Db 163 SAEDILIIITPEPTAIMDAYSAVKHLVLTENKLSMKVAVNRCK-DQKEGLDAFARLSRTI 221

QY 249 --VLDYQEMLSLLGVIPEDSEVIRSNRGPFLVNLNKPPTLAGLAFQAAWRLVRODSM 306
Db 222 HMFIDVQ-----VOPAGSVGDDVIVSKAVVEOVDFFIKSPQAKASRSVRILADALFERET 277

QY 307 K 307
Db 278 R 278

RESULT 14
MRP_SYNY3 STANDARD; PRT; 353 AA.
AC P53383;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MRP PROTEIN HOMOLOG.
GN MRP OR SLR0067.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Suglura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."
RL DNA Res. 2:153-166(1995).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP-BINDING
CC PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D64001; BAA10297.1; -
CC InterPro: IPR002744; DUF59.
CC InterPro: IPR000808; MRP.
CC InterPro: IPR000392; NitrogenaseII.
CC Pfam: PF01883; DUF59; 1.
CC Pfam: PF00142; fer4_NiH; 1.
CC Pfam: PF00142; fer4_NiH; 1.
CC ProbDom: PD005595; DUF59; 1.
CC PROSITE: PS01215; MRP; 1.
KW ATP-binding; Complete proteome.
```


FT NP_BIND 105 112 ATP (POTENTIAL).
SQ SEQUENCE 353 AA; 37131 MW; 891DC0E247113841 CRC64;

Query Match 12.9%; Score 213; DB 1; Length 353;
Best Local Similarity 26.1%; Pred. No. 5e-10;
Matches 82; Conservative 55; Mismatches 115; Indels 62; Gaps 12;

QY 23 KTLISPRFVNPPSRPSIRSVLQFNRRKPELAGETPRIVVITSGKGVGKTTTANVGLS 82

DB 76 KVTAEPTPOOKSLPDQSS-----VGQVKNIIAISGKGVGKSTVAVNVAVA 121

QY 83 LARYGSFVVAIDAGLRLNLDLLGLLENRVNYTCVEVINGDCRLDQALVRDKRWSNFELL 142

DB 122 LAQTGAAGLLDADIYGNAPMTMLGSG----AAVQVQNS----PQGEVLEPVF-NHGIK 172

QY 143 CISKPSKLPKMGF-----GKALEWLVDAKTRPE-CSPDFIIDDPCAGI-DAGF 190

DB 173 MVS-----MGFLIDPDQPVIVRGPMNLGIIIRQFLYQVNWGALDYLVDMPPGTGDAQL 225

QY 191 -ITAITPANEAVLVTPDITALRDVVTGLLECDGIRDIKMIVNR---VRTDMIK--- 242

DB 226 TLTQSVPHAGAVITPTQTVSLDARRGLKMFQMGVNVGLGVENMSYFIPDPLDPRQYD 285

QY 243 -----GEDMMSVLDVQEMGLSLGLGVIPEDSEVIRSTNRGFPVLVKNKPTTLAGLAF 296

DB 286 LFGSGGGEKASKELNV-----PLLCGVPLEIGLREGDGKGVPIVVSQPESASAKALTAI 339

QY 297 AWRLVEQDSMKRVM 310

DB 340 AKQIAGKVSMAALV 353

RESULT 15

MRP_AQUAE STANDARD; PRT: 364 AA.
AC 066946;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE MRP PROTEIN HOMOLOG.
GN MRP OR AQ_737.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL Nature 392:353-358(1998).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: BELONGS TO THE MRP/NBP35 FAMILY OF ATP-BINDING
CC PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE000705; AAC06915.1; -
DR InterPro: IPR00808; Mrp.
DR InterPro: IPR000392; NitrogenaseII.
DR Pfam: PF00142; fer4_NiH; 1.
DR PROSITE: PS01215; MRP; 1.
KW ATP-binding; Complete proteome.

FT NP_BIND 120 127 ATP (POTENTIAL).
SQ SEQUENCE 364 AA; 39492 MW; 320AF95C191A272A CRC64;

Query Match 12.8%; Score 211; DB 1; Length 364;
Best Local Similarity 27.1%; Pred. No. 7.5e-10;
Matches 75; Conservative 50; Mismatches 110; Indels 42; Gaps 10;

QY 35 PSRRSPISRVLQFNRRKPELAGETPRIVVITSGKGVGKTTTANVGLSLARYGFSVVAID 94

DB 96 PQTQOPM-----FTRK-KVPG-VKHIIAVGSGKGVGKSTVAVNVAVALSQGLYKVGVLID 148

QY 95 ADGLRLNLDLLGLLENRVNYTCVEVINGDCRLDQALVRDKRWSNFELLCISKPSKLPWG 154

DB 149 ADVYGPSVPTLFGKLG-----ERVIVD-QFORIIPVEKYGLKLTLSIGFMLPSEDTPII 200

QY 155 FGKAL-EWLVDALKTRPEGSPDFIIDDPCAGIDAGFTAI--TPANEAVLVTTDPDITAI 211

DB 201 WRGPMALKALTEFLSTKWNLDLFDLMDLPPTGVDQVITLAQNVELTGAVVVVTTPODVAL 260

QY 212 RDADRVTLLECDGIRDIKMIVNRVTDMI-----KGEDMMSVLDVQEML 256

DB 261 ADVKAVSM-----FREVNIPLVGLVIENMAYFICPSDKOKYIFGKGR-----VAEFANAY 311

QY 257 GLSLGLVIPEDSEVIRSTNRGFPVLVKNKPTTLAGLAF 293

DB 312 GLKILGISIPIDPEVAEKSDKGEPIVISHPDSEVAKAF 348

Search completed: February 11, 2002, 13:33:23
Job time: 125 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 11, 2002, 13:31:13 ; Search time 16.09 Seconds
(without alignments)
1543.375 Million cell updates/sec

Title: US-09-553-431-2
Perfect score: 1654
Sequence: 1 MASLRLFTNHQSLLLPSSL.....KAVNVEEPPKRGFFSFFGG 326

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	47.9	282	T07303	cell division inhi
2	643	38.9	266	S76970	hypothetical prote
3	573.5	34.7	276	D75478	septum site-determ
4	536.5	32.4	264	C84028	septum site-determ
5	523	31.6	268	G45239	cell division inhi
6	516	31.2	262	F70375	cell division inhi
7	514.5	31.1	269	C82695	septum site-determ
8	506.5	30.6	268	C64561	cell division inhi
9	500.5	30.3	268	B71945	cell division inhi
10	480.5	29.1	271	F83239	cell division inhi
11	479	29.0	270	CECID	cell division inhi
12	479	29.0	270	F85695	hypothetical prote
13	475.5	28.7	271	A72200	septum site-determ
14	468	28.3	276	C82136	septum site-determ
15	460	27.8	270	B84968	septum site-determ
16	449.5	27.2	271	C81230	septum site-determ
17	366	22.1	260	F75175	cell division inhi
18	344.5	20.8	259	B99113	cell division inhi
19	341.5	20.6	245	C71105	probable cell divi
20	335	20.3	263	H69336	cell division inhi
21	327.5	19.8	245	A75056	cell division inhi
22	300	18.1	264	C64368	cell division inhi
23	266	16.1	252	F71191	hypothetical prote
24	262.5	15.9	305	A84363	cell division inhi
25	254	15.4	217	H71038	probable cell divi
26	249	15.1	280	B83463	flagellar synthesi
27	247.5	15.0	251	H75150	cell division inhi
28	246.5	14.9	288	D83954	hypothetical prote
29	243.5	14.7	323	B84251	cell division inhi

30	242	14.6	263	1	B64321	cell division inhi
31	241	14.6	288	2	C81422	probable ATP-bindi
32	239.5	14.5	304	2	D71290	probable ATP-bindi
33	238.5	14.4	295	2	E70133	ATP-binding protei
34	230	13.9	294	2	B64649	ATP-binding protei
35	228	13.8	313	2	B82123	MinD-related prote
36	224	13.5	294	2	D71938	hypothetical prote
37	214	12.9	298	2	I40434	flagellar biosynth
38	213	12.9	353	2	S74379	probable ATPase -
39	211	12.8	364	2	G70364	conserved hypothet
40	209.5	12.7	378	2	E71274	probable ATP-bindi
41	209	12.6	368	2	H71962	hypothetical prote
42	206	12.5	412	2	G64545	ATP-binding protei
43	204.5	12.4	278	2	H70404	cell division inhi
44	202	12.2	297	2	H75132	hypothetical prote
45	197.5	11.9	350	2	F75448	mrp protein - Dein

ALIGNMENTS

RESULT 1

T07303
cell division inhibitor - Chlorella vulgaris chloroplast
C:Species: chloroplast Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07303
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Na
proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga C
A:Reference number: Z15985; MUID:97303241
A:Accession: T07303
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-282 <WAK>
A:Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57951.1; PID:g2224467
C:Genetics:
A:Gene: mind
A:Genome: chloroplast
C:Superfamily: cell division inhibitor mind
C:Keywords: chloroplast

Query Match 47.9%; Score 792; DB 2; Length 282;
Best Local Similarity 60.4%; Pred. No. 4.6e-56;
Matches 165; Conservative 39; Mismatches 55; Indels 14; Gaps 5;
QY 59 RIVVITSGKGVGKTTTANVGLSIARYGFSVVAIDADLGRNLDLLGLNRVNYTCVE 118
DB 17 RVIIVITSGKGVGKTTTANGLMSIARYGVALIDADIGLRNLDLLGLNRVLYTAMD 76
QY 119 VINGDCRLDQALVRDRKWSNFELLCISKPRSKLPMGFGKALEWLVDAKTRPEGSPDFI 178
DB 77 IVEGQCRLDQALIRDRKWNKLLALLAISKNROK--YNYTRKNQNLIDSVK---ELGFOFV 131
QY 179 IIDCPAGIDAGFITAITPANEAVLVTTPDIPALRDADRVTLGLEDGIRDKIMIVNRVRT 238
DB 132 LIDCPAGIDVGFINAIASAQEAIVTTPETAITRADRVAGLLEANGIYNVKLLVNRVRP 191
QY 239 DMKGEDMMSVLDVQEMLGSLGLGVIPEDSEVIRSTNKGFPFLVNLKPPFLAGLAEQAAW 298
DB 192 DMIOKNDMSVRDVOEMLGIPLLGAIPEDSVIISTNKGFLVNLKLLTSLGIAFENAAR 251
QY 299 RLV-EQDSMRVAVVEEPPKRGFF-----SFFGG 326
DB 252 RLIGKQD-----YFIDLTSPPQKMFQKLOEFFLG 280

RESULT 2

S76970
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803

C:\Date: 10-Jun-1993 #sequence_revision 04-Oct-1996 #text_change 19-Jan-2001
 C:\Accession: S31205; C:\Accession: S45239; F45240; A69658; S27521; S29866
 R\Lee, S.; Price, C.W.,
 Mol. Microbiol. 7, 601-610, 1993

Title: The minCD locus of Bacillus subtilis lacks the minE determinant that provides

Accession: S31205

Molecule type: DNA

Residues: 1-268 <LEE>

Cross-references: EMBL:Z15113; NID:g49307; PIDN:CAA78818.1; PID:g580893

Authors: Levin, P.A.; Margolis, P.S.; Setlow, P.; Losick, R.; Sun, D.

Bacteriol. 174, 6717-6728, 1992

Title: Identification of Bacillus subtilis genes for septum placement and shape deter

Reference number: A45239; MUID:93015731

Accession: G45239

Status: not compared with conceptual translation

Molecule type: DNA

Residues: 1-268 <LEV>

Cross-references: GB:M96343; NID:g142852; PIDN:AAA22401.1; PID:g142859

Note: sequence extracted from NCBI backbone (NCBIP:116563)

Varley, A.W.; Stewart, G.C.

J. Bacteriol. 174, 6729-6742, 1992

Title: The divIVA region of the Bacillus subtilis chromosome encodes homologs of Esche

Reference number: A45240; MUID:93015732

Accession: F45240

Molecule type: DNA

Residues: 1-268 <VA2>

Cross-references: EMBL:M95582; NID:g143211; PIDN:AAA22609.1; PID:g143216

Note: sequence extracted from NCBI backbone (NCBIP:116574)

Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berler

Schubert, D.; Bron, S.; Brouillet, C.; Bruschii, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koningsoer, P.; Krogsh, S.; Kumano, M.; Kurita, K.; Lapilus, A.; Lardinof, S.

Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Ogawa, K.; Ogata, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon,

Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot

Tanaka, T.; Terpstera, P.; Togonoi, A.; Tosato, V.; Uchiyama, K.

Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

Reference number: A69580; MUID:98044033

Accession: A69580

Status: nucleic acid sequence not shown; translation not shown

Molecule type: DNA

Residues: 1-268 <KUN>

Cross-references: GB:299118; GB:AL009126; NID:g2635200; PIDN:CAB14759.1; PID:g2635264

Experimental source: strain 168

Genetics:

Gene: TTG

Start codon: TTG

Function:

Description: mediates, together with minC, cell division site selection by specificall

Superfamily: cell division inhibitor mind

Keywords: cell division control; nucleotide binding; P-loop

Region: 10-17/Region: nucleotide-binding motif A (P-loop)

Binding site: ATP (Lys) #status predicted

Query Match 31.6%; Score 523; DB 1; Length 268;
Best Local Similarity 41.1%; Pred. No. 1.5e-34;
Matches 111; Conservative 68; Mismatches 77; Indels 14; Gaps 7;

Dy 61 VVITSGKGVGKTTTANVGLSLARYGFSSVAIDADLGRLNDLLGLLENRVNYTCVEVI 120
:|||||:|||||:|||||: || | :|||:|||||:|||||: |||: |||:
bb 5 IVITSGKGVGKTTTSNLGTALTLGRKRCVLDFDILGNLDVVVYGLNRIIYDLVDV 64
:|||||:|||||:|||||: || | :|||:|||||:|||||: |||: |||:
Dy 121 NGDCRDLQALVRDKRWNSFFELLCISKPKSPMGFGGKALEWLVDALKTRPGSDPFII 180
|||:|||||:|||||: |||: |||: |||: |||: |||: |||: |||:
bb 65 EGRCMKHQALVKDRFDDL-LYLMPAAQTSDKTAVAPGIKNMVQLKQ----EDFYVII 119
|||:|||||:|||||: |||: |||: |||: |||: |||: |||: |||:
Dy 181 DCPAGIDAGTAITPANEAVALVTTPDTIALRDADRVTGLLEC-DGIRDKIMVNVRVT 239
|||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
bb 120 DCPAGIEGYKNVSGADKAIWVPETSAVDADRIIGLTGLEENIEPRIVNVNRH 179
|||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

QY 240 MIKGEDMMSVLDVOEMLGSLGVIPEDSEVIRSTNRGFPVLVNLKPPTLAGLAFEQAAWR 299
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 180 LMKNGTMDIDIEVQHLSIDLLGLIVADDDDEVIKASNHGEPIAMD-PKNRASIATYRNARR 238

QY 300 LYVEQDSMKAVMVVEEPKKRGFF----SFFG 325
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 239 IL-GESVPLOVLEEONK--GMMAKIKSFSG 265

RESULT 6
F70375
cell division inhibitor (septum placement) minD2 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 26-Aug-1999
C:Accession: F70375
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
A:Accession: F70375
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-262 <AQ>
A:Cross-references: GB:AE000712; NID:g2983411; PIDN:AAC06996.1; PID:g2983413; GB:AE00
A:Experimental source: strain VF5
C:Genetics:
A:Gene: mind2
C:Superfamily: cell division inhibitor minD

Query Match 31.2%; Score 516; DB 2; Length 262;
Best Local Similarity 41.4%; Pred. No. 5.2e-34;
Matches 108; Conservative 65; Mismatches 70; Indels 18; Gaps 3;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGSVAIDAIDLGRNLDDLGLLENRVNYTCVEV 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 VVVITSGKGVGKTTTANIGTALAKLGKVKLLIDADIGLRNLDMTLGLENRIVVDILDV 63

QY 120 INGDRLDQALVRDKRWNSFELICISKRSLPMGFGGKALEWLVDALKTRPEGSPDFII 179
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 LEGRVPEKALYDKRKGLSNLLPANQRANKOVIDE-----KWKTVVEIKNSGNWYYIL 119

QY 180 IDCPCAGIAGFITAIIPANEAVLVTPPDITALRDADVDTGLLECGDIRKIMVNRVRTD 239
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 VDSPAIEKGFGQIAVSPADKALIVNPESSIRDADRVTGLLESMDKRYKVIVNRKWE 179

QY 240 MIKGEDMMSVLDVOEMLGSLGVIPEDSEVIRSTNRGFPVLVNLK--PPTLAGLAFEQAA 297
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 180 MVARGAMLSVEDIVDLKAETIGIIPPEPKLVDTNRGEPVLDERKFPASQAII----- 233

QY 298 WRIVEQDSMKAVMVVEEPKKR 318
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 234 -----DTARLMGESIPLKR 248

RESULT 7
C82695
septum site-determining protein XF1321 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: C82695
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen xylella fastidiosa.
A:Reference number: AB2515; MUID:20365717
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: C82695
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <SM>
A:Cross-references: GB:AF003849; NID:g9106133; PIDN:AAF84130.1; GSPDR:GN

A:Experimental source: strain 9a5c

R:Simposon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H. as-Neto, E.; Docena, C.; El-Dorfi, H.; Facincani, A.P.; Ferreira, A.J.S. Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak Rodrigues, V.; Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A5328

A:Contents: annotation

C:Genetics:

A:Gene: XFL321

C:Superfamily: cell division inhibitor mind

Query Match 31.1%; Score 514.5; DB 2; Length 269;

Best Local Similarity 43.5%; Pred. No. 7.1e-34;

Matches 120; Conservative 56; Mismatches 79; Indels 19; Gaps 8;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLLGLLENRVNVTQVEV 119

Db 4 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLLGLLENRVNVTQVEV 63

QY 120 INDCRLDQALVDRKWSNFELLICISPRSKLPMFGGKALEWLDALKTREPGSPDFII 179

Db 64 IDEANTLQALIKDRPDNLYLLAAOTRDKATKEG--VEKVLNELQA--EGP-DYIC 118

QY 180 IDCPAGIDAGFTAITPANEAVLVTPDITATLRDADRVTGLLECDGIRIKI 232

Db 119 CDSFAGTEKASLAMYADRAVYVNVVPEVSSVRSDRIIGLDSKTKAETGGSTITTL 178

QY 233 VNRVDTMIKEDMMSVLDVQEMLSLGLVTPEDSEVIRSTNRGFPVLNKPPTLAGIA 292

Db 179 LTRYSPARVESGEMLSADVEVLGLKAIGVPESGDVLNASKGPEVILDN-NSLAGIA 237

QY 293 FEQAARLVLEQD-SMKAVVVEEPEKRGFFS-FFGG 326

Db 238 YEDAVGRILGEDHPMTTVE----KKGFFSKLFGG 269

RESULT 8

cell division inhibitor mind - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 02-Feb-2001

C:Accession: C64561

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467

A:Accession: C64561

A:Status: preliminary;

A:Molecule type: DNA

A:Residues: 1-268 <TOM>

A:Cross-references: GB:AE000551; NID:g2313430; PIDN:AAD07400.1; PID:g231343

C:Genetics:

C:Function:

A:Description: an ATPase required for correct placement of cell division site

C:Superfamily: cell division inhibitor mind

C:Keywords: ATP; cell division control; nucleotide binding; p-loop

F:10-17/Region: nucleotide-binding motif A (p-loop)

F:16/Binding site: ATP (Lys) #status predicted

Query Match

Best Local Similarity 40.1%; Pred. No. 3.1e-33;

Matches 110; Conservative 65; Mismatches 80; Indels 19; Gaps 5;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLLGLLENRVNVTQVEV 119

Db 4 VVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLLGLLENRVNVTQVEV 63

QY 120 INDCRLDQALVDRKWSNFELLICISPRSKLPMFGGKALEWLDALKTREPGSPDFII 179

Db 64 MEKNCNLSQLITDKTKNLSFLAASQSKDKNLDERKVAI--LINALR----ADFDYIL 117

QY 180 IDCPAGIDAGFTAITPANEAVLVTPDITATLRDADRVTGLLECDGIRIKI 232

Db 118 IDSPAGIESGPEHAILHADLMALVYVTPVSSLRSDRIIGLDSKTKAETGGSTITTL 177

QY 233 VNRVDTMIKEDMMSVLDVQEMLSLGLVTPEDSEVIRSTNRGFPVLNKPPTLAGIA 292

Db 178 INRLKPELVANGEMISIEVLKILCLPLIGIIPEDHIIISATNKGEPI--RTDCESAKA 235

QY 293 FEQAARLVLEQD-SMKAVVVEEPEKRGFFS-FFGG 326

Db 236 YORITRILGEB---VEYVEPKAKRGFFSAUKG 265

RESULT 9

cell division inhibitor - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 26-Aug-1999

C:Accession: B71945

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Daig, P.C.; Smith, D.

IVES, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p

A:Reference number: A71800; MUID:99120557

A:Accession: B71945

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-268 <ARN>

A:Cross-references: GB:AE001468; NID:g4154938; PIDN:AAD05905.1; PID:g415

A:Experimental source: strain J99

C:Genetics:

A:Gene: mind

C:Superfamily: cell division inhibitor mind

Query Match

Best Local Similarity 39.8%; Pred. No. 9.3e-33;

Matches 109; Conservative 65; Mismatches 81; Indels 19; Gaps 5;

QY 60 IVVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLLGLLENRVNVTQVEV 119

Db 4 VVITSGKGVGKTTTANVGLSLARYGFSVVAIDADLGLNLDLLGLLENRVNVTQVEV 63

QY 120 INDCRLDQALVDRKWSNFELLICISPRSKLPMFGGKALEWLDALKTREPGSPDFII 179

Db 64 MEKNCNLSQLITDKTKNLSFLAASQSKDKNLDERKVAI--LINALR----ADFDYIL 117

QY 180 IDCPAGIDAGFTAITPANEAVLVTPDITATLRDADRVTGLLECDGIRI 232

Db 118 IDSPAGIESGPEHAILHADLMALVYVTPVSSLRSDRIIGIIPEDHIIISATNKGEPI--RTDCESAKA 235

QY 233 VNRVDTMIKEDMMSVLDVQEMLSLGLVTPEDSEVIRSTNRGFPVLNKPPTLAGIA 292

Db 178 INRLKPELVANGEMISIEVLKILCLPLIGIIPEDHIIISATNKGEPI--RTDCESAKA 235

QY 293 FEQAARLVLEQD-SMKAVVVEEPEKRGFFS-FFGG 326

Db 236 YORITRILGEB---VEYVEPKAKRGFFSAUKG 265

A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
A; Gene: mind
A; Map position: 26 min
C; Function:
A; Description: a membrane ATPase required for correct placement of cell division site
A; Note: mnc and mind act in concert to form an inhibitor capable of blocking formation found betweenftsZ and mindC
C; Superfamily: cell division inhibitor mind
C; Keywords: ATP; cell division control; nucleotide binding; p-loop
F; 10-17/Region: nucleotide-binding motif A (p-loop)
F; 16/Binding site: ATP (Lys) #status predicted

Query Match 29.0%; Score 479; DB 1: Length 270;
Best Local Similarity 39.9%; Pred. No. 5e-31;
Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;

QY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRNLDDLGLLENRYNYTCVE 118
|||:|||:|||:|||:: : ||: | |||:|||:|||:: : ||| |
Db 3 RIIVVTSGKGVGKTTSSAAIATGLAQKGKTVVIDFDIGLRNLDLIMGCERRVVYDFVN 62
QY 119 VINGDRLDALVRDKRWNSPFELICISKPSKPLPMFGGKALEWLVDALTRPESPDFI 178
|||:|||:|||:|||:: : ||: | |||:|||:|||:: : ||| |
Db 63 VIQGDTALNQALIKDKRTENLYILPASOTRKDALREGVAK--VLDDLKAM---DFEFI 117
QY 179 IIDCPAGIDAGFITAITPANEAFLVTPDITALRDADRVTGLLEC-----DGIRDIK-- 230
: |||:|||:: : ||: | |||:|||:|||:|||:|||:: : ||| |
Db 118 VCDSPAGIETGALMALYFADEAIITPEVSSVRSDSRIILGLASKSRRAENGEEPIKEH 177
QY 231 MIYNVRTDMIKGBDMMSVLDOVMGLGLLGVIPEDSEVIRSTNRGFPVLVKNKPPTLAG 290
::: | ||: | ||: | ||: | |||:|||:|||:|||:|||:: : ||| |
Db 178 LLLTRYNPGRSVRGCDMLSMEDVLEILIKLVGVIPEDQSULRASNOGEPVILDINAD-AG 236
QY 291 LAFEQAARWLVEDOSMKAVMVVEEP-----KKRGFFS-PFGG 326
||: | ||: | ||: | ||: | ||: | ||: | ||: | ||| |
Db 237 KAY-----ADTVERLLGEERPFRFIEEKKGLKLRFGG 270

RESULT 12
F85695
hypothetical protein mind [imported] - Escherichia coli (strain O157:H7)
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C; Accession: F85695
R; Bernal, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimantanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: F85695
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-270 <STO>
A; Cross-references: GB:AE005174; NID:g12514869; PIDN:AAG56026.1; GSPDB:GN00145; UWGP:
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: mind
C; Superfamily: cell division inhibitor mind

Query Match 29.0%; Score 479; DB 2: Length 270;
Best Local Similarity 39.9%; Pred. No. 5e-31;
Matches 113; Conservative 58; Mismatches 82; Indels 30; Gaps 8;

QY 59 RIVVITSGKGVGKTTTANVGLSLARYGSVAIDADGLRNLDDLGLLENRYNYTCVE 118
|||:|||:|||:|||:: : ||: | |||:|||:|||:: : ||| |
Db 3 RIIVVTSGKGVGKTTSSAAIATGLAQKGKTVVIDFDIGLRNLDLIMGCERRVVYDFVN 62
QY 119 VINGDRLDALVRDKRWNSPFELICISKPSKPLPMFGGKALEWLVDALTRPESPDFI 178
|||:|||:|||:|||:: : ||: | |||:|||:|||:: : ||| |
Db 63 VIQGDTALNQALIKDKRTENLYILPASOTRKDALREGVAK--VLDDLKAM---DFEFI 117

QY 179 IIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC-----DCIRDIK-- 230
Db 118 VCDSPAGIETGALMAYFADEAIITNDEVSSVRSDRLTLGLTLAKSRRAENGEEPIKEH 177
QY 231 MIYNVRVTDMKIGEDMMSVLDYQEMGLSLGVLGVPEDSEVIRSTNRGFPVLNKPETLAG 290
Db 178 LLLTFYNNPCVRSGDMSLWEDVLEILTKVLGVIPEDQSVLQASNOCEPVLIDINAD-AC 236
QY 291 LAFOQAAWRLVEQDSMKVAMVEEP-----KKRGFFS-FFGG 326
Db 237 KAY-----ADTVRLGLBERPFRFIEEKKGFLKRLFGG 270

RESULT 13
A72200
septum site-determining protein mind - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: A72200
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
A:Accession: A72200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <ARN>
A:CROSS-references: GB:AE000512; NID:94982455; PIDN:AAD36932.1; PID:9498245
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1870
C:Superfamily: cell division inhibitor mind

Query Match 28.7%; Score 475.5; DB 2; Length 271;
Best Local Similarity 40.9%; Pred. No. 9.5e-31;
Matches 105; Conservative 47; Mismatches 68; Indels 37; Gaps 5;

QY 60 IWVITSGGGVGKTTTANVGLSLARYGSVVAIDADLGLRLNLDLLGLGNRVNVTCEV 119
Db 4 VIVITSGGGVGKTTTANVGLSLARYGSVVAIDADLGLRLNLDLLGLGNRVNVTCEV 63
QY 120 INGCRLDOALVRDKRWSNFELLCISKPSKLPMPGFGGKALEWLDALKTRPEGSDF 175
Db 64 VNGKVPQSEALVKHMLKNLYL-----PASQ-----IATKEMISFNDMK 103
QY 176 -----DFIIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC 225
Db 104 ATVKELIPHFYDIITDSPAGIERGFRNAPAEVLVVTTPDITARDADRVGTGILEC 163
QY 226 IRD--IKMIVNRVTDMKIGEDMMSVLDYQEMGLSLGVLGVPEDSEVIRSTNRGFPVLN 283
Db 164 FSDEKINVIINRFKHKVKGEMLTDDIKHTLSLEITAVIPDSDDIIVASNTGIPVSLN 223
QY 284 KPPTLAGLAFQAAWRL 300
Db 224 GNSRIS-KNFENLARRI 239

RESULT 14
C82136
septum site-determining protein mind vc1960 [imported] - Vibrio cholerae (strain N16961)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82136
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B.
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833

A:Accession: C82136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <HEI>
A:CROSS-references: GB:AE004271; GB:AE003852; NID:9656490; PIDN:AAF95108.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1960
A:Map position: 1
C:Superfamily: cell division inhibitor mind

Query Match 28.3%; Score 468; DB 2; Length 276;
Best Local Similarity 40.4%; Pred. No. 3.9e-30;
Matches 112; Conservative 57; Mismatches 90; Indels 18; Gaps 7;

QY 59 RIIVITSGGGVGKTTTANVGLSLARYGSVVAIDADLGLRLNLDLLGLGNRVNVTCEV 118
Db 9 RIIVITSGGGVGKTTTANVGLSLARYGSVVAIDADLGLRLNLDLLGLGNRVNVTCEV 68
QY 119 VINGCRLDOALVRDKRWSNFELLCISKPSKLPMPGFGGKALEWLDALKTRPEGSDF 178
Db 69 VINGEATLQAALIKDKKNENLFIPLASQTRDKDALTQD--YQVLENDLK---EMGFDEI 123
QY 179 IIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC 225
Db 124 ICDSPAGIEOGALMAYVADAEIIVTNPDEVSSVRSDRLTLGLTLAKSRRAENGEEPIKEH 183
QY 231 MIYNVRVTDMKIGEDMMSVLDYQEMGLSLGVLGVPEDSEVIRSTNRGFPVLNKPETLAG 290
Db 184 LILTRNPARVTCQEMLSVQDVEEILHVLLGVIPESQAVLNASNGVPIFDQSD-AC 242
QY 291 LAFOQAAWRLV-EQDSMKVAMVEEPKKRGFFSFFGG 326
Db 243 QAYQDTVARLLGQVEFREL---TEAKGIFKRLFGG 276

RESULT 15
B84968
septum site-determining protein mind [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: B84968
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
A:Reference number: A84930; MUID:20445173
A:Accession: B84968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <STO>
A:CROSS-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: mind; BU326
C:Superfamily: cell division inhibitor mind

Query Match 27.8%; Score 460; DB 2; Length 270;
Best Local Similarity 38.3%; Pred. No. 1.6e-29;
Matches 106; Conservative 60; Mismatches 91; Indels 20; Gaps 5;

QY 59 RIIVITSGGGVGKTTTANVGLSLARYGSVVAIDADLGLRLNLDLLGLGNRVNVTCEV 118
Db 3 RIIVITSGGGVGKTTTANVGLSLARYGSVVAIDADLGLRLNLDLLGLGNRVNVTCEV 62
QY 119 VINGCRLDOALVRDKRWSNFELLCISKPSKLPMPGFGG--KALEWLDALKTRPEGSDF 176
Db 63 VIQGDATLQAALIKDKKNENLFIPLASQTRDKDALTFRIGVKEKVLTEI-----KWNFD 115
QY 177 FIIDCPAGIDAGFITAITPANEAVLVTTPDITARDADRVGTGILEC 225
Db 116 FIIDCPAGIETGALMAYFADEAIITNDEVSSVRSDRLTLGLTLAKSRRAENGEEPIKEH 175

QY 231 --MIVNVRVTDMIKEDMMSVLDVQEMLSLGLGVTPEDSEVIRSTNRGFPPLVNLKPPTL 288
Db 176 EYLLLTRYNPRVRKKGEMLSMTDVLQIPITIGVIPEDQSVLRASNOGESIILDINSN - 234
QY 289 AGLAFEAQAAWRLVEQDSMKAVWVEEPKKRGFSFPG 325
Db 235 ACAYSDTVNRLGEE--RHFRFIEEEKSFLLRRLFG 269

Search completed: February 11, 2002, 13:33:03
Job time: 110 sec